

10/588542

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SEQUENCE LISTING

<110> EISAI CO., LTD.

<120> Screening method

<130> E1-A0410Y1P

<150> JP 2004-31591

<151> 2004-02-09

<150> JP 2004-368509

<151> 2004-12-20

<160> 14

<170> PatentIn version 3.1

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<220>

<221> CDS

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Gly Glu Leu Trp Pro Gly Ala Glu Ala Arg Ala Ala Pro Tyr Gly Val
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agg ctt tgc ggc cga gaa ttc atc cga gca gtc atc ttc acc tgc ggg 144
Arg Leu Cys Gly Arg Glu Phe Ile Arg Ala Val Ile Phe Thr Cys Gly
35 40 45

ggc tcc cgg tgg aga cga tca gac atc ctg gcc cac gag gct atg gga 192
Gly Ser Arg Trp Arg Arg Ser Asp Ile Leu Ala His Glu Ala Met Gly
50 55 60

gat acc ttc ccg gat gca gat gct gat gaa gac agt ctg gca ggc gag 240
Asp Thr Phe Pro Asp Ala Asp Ala Asp Glu Asp Ser Leu Ala Gly Glu

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85	90	95		
ccc cag gcc ttt tac agg ggg cga ccc agc tgg caa gga acc cct ggg Pro Gln Ala Phe Tyr Arg Gly Arg Pro Ser Trp Gln Gly Thr Pro Gly				336
100	105	110		
gtt ctt cgg ggc agc cga gat gtc ctg gct ggc ctt tcc agc agc tgc Val Leu Arg Gly Ser Arg Asp Val Leu Ala Gly Leu Ser Ser Ser Cys				384
115	120	125		
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Gly Ser Arg Trp Arg Arg Ser Asp Ile Leu Ala His Glu Ala Met Gly			
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85	90	95	

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gag gcg gcc aac acg agt ggt aac gcg tcg ctg cag ctt ccg gac ttg Glu Ala Ala Asn Thr Ser Gly Asn Ala Ser Leu Gln Leu Pro Asp Leu	504
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gcg ggc aac ctg ctg gtt ctc tac ctg atg aag agc atg cag ggc tgg Ala Gly Asn Leu Leu Val Leu Tyr Leu Met Lys Ser Met Gin Gly Trp	696
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cgc aag tcc tct atc aac ctc ttc gtc acc aac ctg gcg ctg acg gac Arg Lys Ser Ser Ile Asn Leu Phe Val Thr Asn Leu Ala Leu Thr Asp	744
115 120 125	
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180 185 190	
acc cga gga cac ggc cgg ggc gac tgc tgc ggc cgg agc ctg ggg gac Thr Arg Gly His Gly Arg Gly Asp Cys Cys Gly Arg Ser Leu Gly Asp	984
195 200 205	
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ggc cgc gac agg cag ttc tgg ctg ggc ctc tac cac tcg cag aag gtg Gly Arg Asp Arg Gln Phe Trp Leu Gly Leu Tyr His Ser Gln Lys Val	260	265	270	1176	
ctg ttg ggc ttc gtg ctg ccg ctg ggc atc att atc ttg tgc tac ctg Leu Leu Gly Phe Val Leu Pro Leu Gly Ile Ile Ile Leu Cys Tyr Leu	275	280	285	1224	
ctg ctg gtg cgc ttc atc gcc gac cgc cgc gcg ggg acc aaa gga Leu Leu Val Arg Phe Ile Ala Asp Arg Arg Ala Ala Gly Thr Lys Gly	290	295	300	1272	
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ctg tgt tgg ctg ccc aac cag gcg ctc acc acc tgg agc atc ctc atc Leu Cys Trp Leu Pro Asn Gln Ala Leu Thr Thr Trp Ser Ile Leu Ile	340	345	350	1416	
aag ttc aac gcg gtg ccc ttc agc cag gag tat ttc ctg tgc cag gta Lys Phe Asn Ala Val Pro Phe Ser Gln Glu Tyr Phe Leu Cys Gln Val	355	360	365	1464	
tac gcg ttc cct gtg agc gtg tgc cta gcg cac tcc aac agc tgc ctc Tyr Ala Phe Pro Val Ser Val Cys Leu Ala His Ser Asn Ser Cys Leu	370	375	380	1512	
aac ccc gtc ctc tac tgc ctc gtg cgc cgc gag ttc cgc aag gcg ctc Asn Pro Val Leu Tyr Cys Leu Val Arg Arg Glu Phe Arg Lys Ala Leu	385	390	395	400	1560
aag agc ctg ctg tgg cgc atc gcg tct cct tcg atc acc agc atg cgc Lys Ser Leu Leu Trp Arg Ile Ala Ser Pro Ser Ile Thr Ser Met Arg	405	410	415	1608	
ccc ttc acc gcc act acc aag ccg gag cac gag gat cag ggg ctg cag Pro Phe Thr Ala Thr Thr Lys Pro Glu His Glu Asp Gln Gly Leu Gln	420	425	430	1656	

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 Ala Pro Ala Pro Pro His Ala Ala Glu Pro Asp Leu Leu Tyr Tyr
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cca cct ggc gtc gtg gtc tac agc ggg ggg cgc tac gac ctg ctg ccc 1752
 Pro Pro Gly Val Val Val Tyr Ser Gly Gly Arg Tyr Asp Leu Leu Pro
 450 455 460

agc agc tct gcc tac tga cgcaaggcctc aggcccaggg cgccgcgtcg 1800
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 35 40 45

Trp Trp Glu Leu Gly Leu Glu Leu Pro Asp Gly Ala Pro Pro Gly His
 50 55 60

Pro Pro Gly Ser Gly Ala Glu Ser Ala Asp Thr Glu Ala Arg Val
 65 70 75 80

Arg Ile Leu Ile Ser Val Val Tyr Trp Val Val Cys Ala Leu Gly Leu
 85 90 95

Ala Gly Asn Leu Leu Val Leu Tyr Leu Met Lys Ser Met Gln Gly Trp

100

105

110

Arg Lys Ser Ser Ile Asn Leu Phe Val Thr Asn Leu Ala Leu Thr Asp
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Phe Gin Phe Val Leu Thr Leu Pro Phe Trp Ala Val Glu Asn Ala Leu
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Asp Phe Lys Trp Pro Phe Gly Lys Ala Met Cys Lys Ile Val Ser Met
145 150 155 160

Val Thr Ser Met Asn Met Tyr Ala Ser Val Phe Phe Leu Thr Ala Met
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180 185 190

Thr Arg Gly His Gly Arg Gly Asp Cys Cys Gly Arg Ser Leu Gly Asp
195 200 205

Ser Cys Cys Phe Ser Ala Lys Ala Leu Cys Val Trp Ile Trp Ala Leu
210 215 220

Ala Ala Leu Ala Ser Leu Pro Ser Ala Ile Phe Ser Thr Thr Val Lys
225 230 235 240

Val Met Gly Glu Glu Leu Cys Leu Val Arg Phe Pro Asp Lys Leu Leu
245 250 255

Gly Arg Asp Arg Gin Phe Trp Leu Gly Leu Tyr His Ser Gin Lys Val
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275 280 285

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290

295

300

Gly Ala Ala Val Ala Gly Gly Arg Pro Thr Gly Ala Ser Ala Arg Arg
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325 330 335

Leu Cys Trp Leu Pro Asn Gin Ala Leu Thr Thr Trp Ser Ile Leu Ile
340 345 350

Lys Phe Asn Ala Val Pro Phe Ser Gin Glu Tyr Phe Leu Cys Gin Val
355 360 365

Tyr Ala Phe Pro Val Ser Val Cys Leu Ala His Ser Asn Ser Cys Leu
370 375 380

Asn Pro Val Leu Tyr Cys Leu Val Arg Arg Glu Phe Arg Lys Ala Leu
385 390 395 400

Lys Ser Leu Leu Trp Arg Ile Ala Ser Pro Ser Ile Thr Ser Met Arg
405 410 415

Pro Phe Thr Ala Thr Thr Lys Pro Glu His Glu Asp Gin Gly Leu Gin
420 425 430

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<211> 83

<212> DNA

<213> Artificial Sequence

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<223> A sense strand for CREx2hb

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gtatgacggc catggggatc ccg 83

<210> 9

<211> 83

<212> DNA

<213> Artificial Sequence

<220>

<223> An antisense strand for CREx2hb

<400> 9

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tcgaattcga tatcaagctt ggg 83

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<211> 78

<212> DNA

<213> Artificial Sequence

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ggagccttc tcttactccc aggacttcag cacctaagac agctccaaaa caaaccagaa	240
cagtcagctc cgacctgcag tgca	264